DETAILED ACTION

Continued Examination Under 37 CFR 1.114

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 7/6/2009 and 8/11/2009 have been entered.

Claim Status and Formal Matters

This action is in response to papers filed 8/11/2009.

Claims 2, 4-5, 9, 13, 16-19, 23, 28-30, 32-35 are pending.

Claims 16-19, 23, 28-30, 32-35 have been withdrawn.

The 102 of Ahr has been withdrawn as Ahr does not teach the claimed probes.

The sequence compliance objection has been withdrawn, as the disclosure has met the sequence compliance requirements. It is noted that due to the discrepancies between the numerous amendments of the specification and sequence listing as well as the non-entry of the amendment by the international search authority the specification appears to contain new matter.

The interview record is complete based on applicant's submission.

The IDS submitted 7/6/2009 has been considered.

Claims 2, 4-5, 9, 13 are under examination.

Priority

The instant application was filed 5/1/2006 and is a national stage entry of PCT/GB03/05102 filed 11/21/2003 and claims priority to United Kingdom Patent Application 0227238.3 filed on 11/21/2002.

Specification-New Grounds

2. The amendment filed 10/3/2008 and 7/6/2009 is objected to under 35 U.S.C. 132(a) because it introduces new matter into the disclosure. 35 U.S.C. 132(a) states that no amendment shall introduce new matter into the disclosure of the invention. MPEP 2163.07 II states:

An amendment to correct an obvious error does not constitute new matter where one skilled in the art would not only recognize the existence of the error in the specification, but also recognize the appropriate correction. In re Odd, 443 F.2d 1200, 170 USPQ 268 (CCPA 1971).

The added material which is not supported by the original disclosure is as follows:

The amended table 1a of 10/3/2008 lists clone ID I-24 as having 371 nucleotides and corresponding to SEQ ID NO11. The specification of 5/19/2005 lists in table 1a that I-24 is SEQ ID 308 and also has 373 nucleotides. SEQ ID NO 11 and SEQ ID NO 308 although having the same number of nucleotides have different sequences. Further the amendment of 10/3/2008 lists clone ID V-61 as SEQ ID NO 308 and the specification of 5/19/2005 lists V-61 as SEQ ID NO 721. Thus the amendment of 10/3/2008 has entered New Matter in the specification as the 10/3/2008 specification has changed numerous nucleotide sequence exemplified by I-24 and V-61, above and the artisan

would not recognize the obvious error in the specification as the previous SEQ ID NO corresponded to sequences present in the CRF of the disclosure. Further there is nothing of record suggesting that switching the SEQ ID NO is an obvious correction.

The response and interviews have put forth an amendment to the specification accompanied the International patent examination report as filed on 5/19/2005. This amendment was not entered by the international search authority as it was viewed as new matter. Thus this is not viewed to provide support to the amendments to the specification that have been submitted.

The amendment that has been presented is not consistent with the sequence listing as noted below:

The specification as amended on 7/6/2009 states that SEQ ID NO 399 has 156 nucleotides, while the sequence listing teaches it is 155 nucleotides.

Further the specification in table 1a also teaches that SEQ ID NO 36 is 528 nucleotides, while the sequence listing states it is 527 nucleotides. Further the specification teaches that SEQ ID NO 500 is 382 nucleotides, while the sequence listing teaches it is 556 nucleotides. Further the specification in table 1a teaches that SEQ ID NO 499 is 421 nucleotides, while the sequence listing teachings it is 392 nucleotides. Further the specification teaches SEQ ID NO 270 is 691 nucleotides while the sequence listing teaches it is 591. Further the specification teaches SEQ ID No 337 is 601 nucleotides, while the sequence listing teaches it is 501 nucleotides. The specification appears to assert the length of SEQ ID NO 388 is not known as the length is blank in table 1a, however the sequence listing teaches it is 561 nucleotides.

Further instant table 1 a has deleted references to 156 clones including but not limited to ID I-01, I-02, I-13 are informative for disease diagnosis. This deletion appears to contradict the initial disclosure that these probes were informative, thus changing the scope of the disclosure.

Further Table 2 b has deleted references to clone 60 clone ID including I-52 are informative for diagnosis of breast cancer. This deletion appears to contradict the initial disclosure that these probes were informative, thus changing the scope of the disclosure. Additional as described for table 1 the clone ID of the instant amendment now correspond to different SEQ ID NO.

Further table 3 has deleted reference to reference 60 clone ID including all those listed for the 30% level in the specification of 5/19/2005. This deletion appears to contradict the initial disclosure that these probes were informative, thus changing the scope of the disclosure. Additional as described for table 1 the clone ID of the instant amendment now correspond to different SEQ ID NO. Further the amendment of table 3 appears to make table 6 inconsistent with the data of table 3, as table 6 states that 23 probes were informative with 100% occurrence, while amended table 3, presents only 14 probes that are informative. Thus as the amendment has deleted probes from table 3 at 100%, 80%, 70%, 50%, 40%, 20%, 10%, and in at least one model the amendment has significantly change the disclosure and has provided numerous in consistencies. Further the text has not been amended to reflect the deletion of the sequences, thus the amendment has made the tables and text in consistent.

Further Table 4a has deleted references to clone 103 clone ID including I-01, I-02, I-03 are informative for diagnosis of Alzheimer's in the specification of 5/19/2005. This deletion appears to contradict the initial disclosure that these probes were informative, thus changing the scope of the disclosure. Additional as described for table 1 the clone ID of the instant amendment now correspond to different SEQ ID NO.

The instant amendment to table 4 b has changed the SEQ ID NO associated with each clone ID similar to as was done Table 1

The instant amendment to table 9 has changed the SEQ ID NO associated with each clone ID similar to as was done Table 1

Thus as all the deletions of clone ID NO and switching of SEQ ID NO was not an obvious error nor are the deletions or switching of SEQ ID NO obvious corrections, the amendments are new matter. The amendment has changed the disclosure of the invention in such a way that was not supported by the specification at time of filing.

Applicant is required to cancel the new matter in the reply to this Office Action.

Response to Arguments

The response traverses the New Matter Objection. The response and interview summary of 8/11/2009 asserts that the amendment to correlate the sequences of the specification with those of the sequence listing was based upon the amended pages submitted with International preliminary Examination Report and these correspond to the substitute sequence listing submitted May 1, 2006. These arguments have been thoroughly reviewed but are not considered persuasive as the amended sheets submitted with the IPER were not entered by the international search authority as the

International search authority viewed the amendment to contain new matter. Thus the amended sheets provided with the IPER do not provide support for the correction until there is a demonstration that the amended sheets do not contain New matter relative to the application as filed with WIPO.

Further the amendment as described in more detail above present's inconsistencies between the length of the nucleotide sequences as described in the tables, the prior amendments and the sequence listing. Thus these inconsistencies in conjunction with the New matter issue raised by the international searcher strengthen the New matter rejection with respect to the sequence issues.

Finally the amendment to the specification to eliminate clone Ids from the various tables has been addressed by the response by asserting invention is the sequences that have been provided and there is not a removal of sequences that were never disclosed. These arguments have been thoroughly reviewed but are not considered persuasive as this aspect of the New matter rejection is not drawn to the removal of sequences, but the initial disclosure described numerous informative probes that resulted in a certain specificity, sensitivity, and accuracy as disclosed in Table 6. Table 6 states that in 100% of cases examined a set of 23 probes with informative with an 84.78% specificity, 75.86% sensitivity, 81.33% accuracy and 18.67% error rate. The specification in the application as filed recites 23 clone ID in table 3, however, the amended table recites only 14, as 9 have been deleted. Thus the amendment has altered the scope of the disclosure thus providing numerous inconsistencies in table 3

and table 6 as well as the specification as the specification has not been amended to be consistent with the tables as amended.

Claim Rejections - 35 USC § 112

3. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

4. Claims 2, 4-5, 9 and 13 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. This rejection is drawn to the use of the claimed 351 oligonucleotide probes.

There are many factors to be considered when determining whether there is sufficient evidence to support that a disclosure does not satisfy the enablement requirement and whether any necessary experimentation is undue. These factors have been described by the court in re Wands, 8 USPQ2d 1400 (CA FC 1988). Wands states at page 1404,

"Factors to be considered in determining whether a disclosure would require undue experimentation have been summarized by the board in the Ex parte Forman. They include (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence of working examples, (4) the nature of the

invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims."

The nature of the invention and the breadth of the claims:

Amended claim 2 is drawn to a set of oligonucleotide probes consisting of not more than 1000 oligonucleotides and said set comprising the 351 oligonucleotides having the sequences set forth in the recited SEQ ID NO, with the proviso that at least one of said 351 oligonucleotides may be replaced with either (i) an oligonucleotide fragment of the one of said 351 oligonucleotides being replaced, which fragment is at least 15 nucleotides in length; (ii) an oligonucleotide having a sequence entirely complementary to the one of said 351 oligonucleotide being replaced, or to a fragment thereof which is at least 10 nucleotides in length or (iii) an oligonucleotide having at least 80% identity to the one of said 351 oligonucleotide being replaced or to a fragment thereof which is at least 20 nucleotides in length.

For the specification to be enabling for the set of oligonucleotide probes claimed, it must teach how to use the probe set for diagnosis of disease.

The amount of direction or guidance and the Presence and absence of working examples.

The specification, "different sets of probes may be used in techniques to prepare gene expression patterns and identify, diagnose or monitor different states, such as diseases, conditions or stages thereof" (see page 1, 1st paragraph).

The specification teaches, "we now describe probes and sets of probes derived from cells which are not disease cells and which have not

contacted disease cells, which correspond to genes which exhibit altered expression in normal versus disease individuals, for use in methods of identifying, diagnosing or monitoring certain conditions, particularly diseases or stages thereof" (see last paragraph page 4 to top of page 5).

Example 1 of the specification teaches on page 64 that 497 genes were eliminated and 938 genes remained that were normalized to different external controls (page 65). The specification teaches that correct prediction was obtained in most breast cancer cell lines (page 65). The specification teaches on page 65 that this model correctly identified 41 of 46 non cancer samples (page 65). Thus example 1 of the instant specification suggests that 938 genes can be used to identify breast cancer. It is noted that the specification does not specifically recite with respect to example 1 which 938 probes were informative. Further is noted that Table 6 asserts that from 23 to 139 probes were used as diagnostic, but states an error rate of between 13 and 20%.

Example 2 of the specification teaches that an array of 758 cDNA clones were used instead of the 1435 probes in example 1 (page 67). The specification does not teach the number of the 758 cDNA clones required to be predictive, but notes in table 7 that none of the 14 subjects analyzed were predicted to have Alzheimer's by the method.

Example 3 of the specification a classification model that is generated by using 719 cDNA (page 71). The specification teaches that 111 of the 719 cDNA are described in Table 2 (page 71).

Example 3 of the specification teaches that 730 cDNA clones were picked and 520 probes were sequenced (page 73).

The specification does not provide examples of replacing any SEQ ID NO with fragments of cited SEQ ID NO or sequences that are 80% identical to the fragments.

The specification teaches that SEQ ID NO 268 is a 683 nucleotide sequence with numerous N (degenerate nucleotides) including a long stretch from position 506 to 514, 516 to 524, and 527 to 540.

The specification teaches that SEQ ID NO 389 a sequences of 601 nucleotides that has numerous N (degenerate nucleotides) including at positions 16-20, 87-89, 91-94, 120-122, 129-130, 228-229, 261-263, 267-268, 278-279.

The state of prior art and the predictability or unpredictability of the art:

The art of Cheung et al (Nature Genetics, 2003, volume 33, pages 422-425) teaches that there is natural variation in gene expression among different individuals. The reference teaches an assessment of natural variation of gene expression in lymphoblastoid cells in humans, and analyzes the variation of expression data among individuals and within individuals (replicates) p.422, last paragraph; Fig 1). The data indicates that, for example, expression of ACTG2 in 35 individuals varied by a factor of 17; and that in expression of the 40 genes with the highest variance ratios, the highest and lowest values differed by a factor of 2.4 or greater (Fig 3).

The unpredictability of correlating gene expression level to any phenotypic quality is taught in the prior art of Wu (Journal of Pathology, 2001, volume 195, pages 53-65). Wu teaches that gene expression data must be interpreted in the context of other

biological knowledge, involving various types of 'post genomics' informatics, including gene networks, gene pathways, and gene ontologies (p.53, left col.). The reference indicates that many factors may be influential to the outcome of data analysis, and teaches that expression data can be interpreted in many ways. The conclusions that can be drawn from a given set of data depend heavily on the particular choice of data analysis. Much of the data analysis depends on such low-level considerations as normalization and such basic assumptions as normality (p.63 - Discussion). The prior art of Newton et al (Journal of Computational Biology, 2001, volume 8, pages 37-52) further teaches the difficulty in applying gene expression results. Newton et al teaches that a basic statistical problem is determining when the measured differential expression is likely to reflect a real biological shift in gene expression, and replication of data is critical to validation (p.38, third full paragraph).

Draghici et al (Trends in Genetics (2006) volume 22, pages 101-109) that shortening probes from 30 nucleotides to 25 nucleotides reduces the sensitivity 10 fold (page 103, 1st column, 1st full paragraph). Draghici teaches that splice variant introduce variation in microarrays as short probes to not correctly identify the expression of all splice variants , while long probes will detect all variants (page 107, 2nd Column, 2nd paragraph). Draghici teaches that a limited amount of complementarity can be sufficient to enable binding of two unrelated sequences (page 107, 2nd column, last paragraph).

The level of skill in the art:

The level of skill in the art is deemed to be high.

Quantity of experimentation necessary:

In order to practice the invention as claimed, one would first have to determine if one of skill in the art could make and predictably use the invention as claimed. Thus the artisan would have to determine if the claimed collection of oligonucleotides would allow detection or diagnosis of breast cancer or Alzheimer's as asserted in the specification.

It would be unpredictable in that the artisan would first have to determine which nucleic acids are informative in the instant method. This would be unpredictable in view of the New Matter objection. The specification filed on 5/19/2005 suggested informative probes identified by clone IDs and SEQ ID NO in the tables; the amendment of 10/3/2008 and 7/6/2009 identifies clone ID No correspond to different SEQ ID NO. Further the amendment has deleted reference to over 100 clones, suggesting these clones are not informative, contrary to the initial filing. Further the amendment has presented the nucleic acid sequences of reference have different lengths then disclosed in previously presented amendments as well as the sequence listing. It would thus be unpredictable to use a collection of probes for detection or diagnosis of a disease without knowledge of which probes are truly informative and certainty the probes claimed are actually those viewed as informative.

It would be unpredictable to use a probe that is only 20 nucleotides in length and at least 80% identical to the claimed sequences as SEQ ID NO 73, has 19 Ts at position 222-240 and thus would hybridize with every poly-adenylated mRNA. Further the first 19 nucleotides of SEQ ID NO 340 are also T and would have the same affinity for polyA mRNA. SEQ ID NO 441 also has the first 18 nucleotides as poly T, while SEQ ID NO 472 has over 105 thymines in the first 110 nucleotides. Thus as the sequence

claimed contain fragments of 20 nucleotides with 80% identity that would hybridize every polyA tails it would be unpredictable to practice the invention as claimed. Further in view of the teachings of Draghici it would be unpredictable to use shorter probes to detect longer sequences without specific guidance that the claimed probes would specifically hybridize to only sequence complementary to the full SEQ ID NO and thus identify the nucleotide sequence that allows for diagnosis.

This would be replete with unpredictable trial and error analysis because the specification does not how the expressed probe set is used to diagnose disease. Specifically the specification has in tables 1a, 1b, 2a, 2 b, 4 and 9 of the specification identify sequences that are informative of a disease state, breast cancer, Alzheimer's or Alzheimer's and breast cancer, however the specification does not teach how the combination of SEQ ID NO diagnose Alzheimer's or breast cancer. Thus the skilled artisan would have to determine if all the claimed capture probes or a specific subcombination of probes would have to demonstrate an increase or decrease expression to result in the diagnosis of any disease or Alzheimer's or breast cancer. This would be further unpredictable as the various tables do not recite that the claimed genes are informative.

Response to Arguments

As noted with the first point of the arguments, the claims are not viewed as enabled due to the New matter issues that have been addressed previously. The examiner concurs that obviating the New Matter objection, will substantially decrease the issues involved in this case.

The examiner notes that claims requiring the entire sequence of the probes may be enabled if the new matter issues can be overcome. However, the response appears to misunderstand the other aspects of the previous rejection. The issues previously were the claims could be interpreted to require replacing any probe with any other sequence that was at least 20 nucleotides in length. It did not necessarily require the probe be from the sequence being replaced.

The other issue is the claims are drawn to the use of any fragment of the claimed SEQ ID NO that is at least 20 nucleotides of the SEQ ID NO being replaced, or at least 20 nucleotides and completely complementary to the sequence being replaced, or at least 80% identity to the sequence being replaced or a fragment thereof. Thus for the claimed array to allow for predictable diagnosis of Alzheimer's or breast cancer probes that are less than the full length would have to be specific to the whole sequence of the SEQ ID NO. In the instant case there are at least 4 probes that have fragments that comprise over 80% thymines and thus would base pair with almost every poly A tail and thus would not be specific for the full length SEQ ID NO claimed. Further the specification has provided no indication that every or any 20 base fragment of a SEQ ID NO would allow specific detection of the full length sequences taught by the specification to be indicative of differential expression patterns. Draghici was specifically brought forth to demonstrate that the art recognizes that shorter probes may not detect expression of mRNA if the probe is directed to a part of the message that can be part of a splice variant. Further shorter sequences may hybridize to sequences that

have homology to the mRNA of interest but are not the mRNA detected by the larger probes.

The response on page 42 continues to traverse the rejection by noting that the rejection is based on the scope of the invention. The examiner concurs that if the new matter issues can be overcome and the claims are limited to probes of the length disclosed as used in the specification this aspect of the rejection may be withdrawn. However, based on the teachings of Draghici, the fact multiple probes as claimed as fragments would specifically hybridize to poly-A tails and the lack of any teachings by the specification that such substitution of any fragment of at least 20 nucleotides as claimed would predictably work the claims are viewed as unpredictable.

The response then reviews the issues with Table 7, before moving on to the teachings of Orr. The response asserts that the office's position is whether breast cancer or Alzheimer's disease can be predictably detected by microarray data. This argument has been reviewed but is not considered persuasive as the position is that microarray analysis as presented in the specification may allow for the determination of an increased likelihood of Alzheimer's disease or breast cancer, however, the claims include fragments that may result in detection of splice variants or other transcripts due to the shorter probes or fragments claimed that would not be predictable based on the poly-T sequences and the teachings of Draghici.

The arguments to the New matter issues are not persuasive for the reasons described above.

The response asserts that Table 6 allows for the use of between 23 and 139 probes that allow for a diagnostic error rate of 13 to 20%. However, the specification as amended in table 3 no longer teaches the same number of probes are informative. Specifically Table 3 now recites 14 probes are informative with 100% occurrence, while table 6 states 23 probes. Thus the amendment of the specification has resulted in inconsistencies and thus unpredictability. Thus the skilled artisan upon reading the specification from table 3 would believe only 14 probes are informative with 100% occurrence, while table 6 indicates 23 are informative. Thus it would be unpredictable to practice the invention as claimed with the instant amendment to the specification. Further it is noted that the amendment to the specification has deleted reference to the Clone ID without sequences, it would be unpredictable to practice the invention without this knowledge as the specification appears to teach these clones were part of the diagnosis process.

The response argues the assertions of the Office action asserting 182 probes can be used to predict Alzheimer's disease. These arguments have been thoroughly reviewed but are not considered persuasive as Table 4 a lists 78 informative probes that are used for diagnosis or Alzheimer's disease and while table 4 b recites over 400 probes in view of the amendment of 10/3/2008. Thus contrary to the assertions of the response the artisan would not know which probes to use either the 78 probes of table 4a or the over 400 probes of 4b. In either case neither table teaches 182 probes are used in classification. While the text of the specification may recite that 182 probes were used, the artisan would have to use the tables to determine which probes are

required. Thus based on the inconsistencies of the disclosure the artisan would not know the number of probes required or which probes are required for diagnosis.

The response moves to example 3 and asserts the on page 69 (which is actually page 71 of 10/3/2008 amendment) is drawn to the analysis of 111 probes in table 2 or 345 probes. Again, the assertion of the response appears to be inconsistent with the specification amendment of 10/3/2008 in which table 2a has 77 probes, while table 2b has 351. Thus the artisan based on the discrepancies of the disclosure would not know which probes are required or the number of probes that are informative.

The response continues arguments to example 3 by asserting the 6 additional probes would make little difference. These arguments have been thoroughly reviewed but are not considered persuasive as the claims are not limited to the full length probes as discussed previously. In addition there are discrepancies in the number of probes required depending on the table used and finally there is no indication which SEQ ID NO need to be unregulated or down regulated to allow for diagnosis.

The response continues to argue the declaration and asserts that 6 additional probes does not sufficiently change the efficacy. These arguments may be persuasive if the specification clearly identified which probes must be associated with up regulation or down regulation as well as clearly indicated which probes are required and was consistent in these assertions. However the text of the specification appears to be inconsistent with the table presented and does not clearly indicate which probes are required and the differential expression required at those probes.

Thus the specification contrary to the assertions is not enabling for the full scope of the claimed inventions.

The response continues by asserting the use of fragments will allow for detection of "same transcripts" and thus allow relevant detection. These are arguments that have not been supported by evidence. As stated in the MPEP, 2106 "Arguments of Counsel"

"However, it must be emphasized that arguments of counsel alone cannot take the place of evidence in the record once an examiner has advanced a reasonable basis for questioning the disclosure. See In re Budnick, 537 F.2d at 538, 190 USPQ at 424; In re Schulze, 346 F.2d 600, 145 USPQ 716 (CCPA 1965); In re Cole, 326 F.2d 769, 140 USPQ 230 (CCPA 1964). For example, in a case where the record consisted substantially of arguments and opinions of applicant's attorney, the court indicated that factual affidavits could have provided important evidence on the issue of enablement."

This should not be construed as an invitation for providing evidence.

Further the teachings of Draghici as well as several probes that contain long stretches of poly-T suggests that this is not necessarily true. A polynucleotide sequence with only poly T would not necessarily bind the same sequence. Further the response has asserted that the fragments would hybridize the same splice variants, but again has provided no evidence. Thus these arguments are not persuasive.

The response again brings up the Orr reference. The examiner again concurs that microarray analysis is known and is predictable, if using the same array and a specific hybridization pattern is disclosed. The instant specification has merely provided probes that allow for differential expression, but does not disclose any hybridization pattern. Further Orr does not address the use of fragments or the inconsistencies in the specification. Thus it would be unpredictable to use fragments without specific evidence that the fragments detect only the same sequence as the full length probes.

The response again mischaracterizes the arguments with respect to Draghici. Draghici is not presented to assert that using microarray has to be clinically verified, but the use of probes other than those shown to work, must be verified such as the fragments claimed. The applicant's have not demonstrated that the fragments predictably bind the same mRNA and thus are unpredictable based on the teachings of Draghici. Further the response cannot be predicted as the claims nor specification indicate which probes allow for proper detection and thus diagnosis.

The arguments to the claims requiring the mRNA bind the same splice variants is moot in view of the amendment of 8/11/2009.

The rejection is thus maintained in view of the arguments presented above.

Summary

No claims are allowed.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to STEVEN C. POHNERT whose telephone number is (571)272-3803. The examiner can normally be reached on Monday-Friday 6:30-4:00, every second Friday off.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, James (Doug) Schultz can be reached on 571-272-0763. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Steven C Pohnert/
Examiner, Art Unit 1634

Steven Pohnert